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TABLE I

Class	Strain	Gene	Similarity to:		Known or Putative Function:	In vitro CI:	In vivo CI:
			%	Span			
Cell Surface	9C2	cpxC			capsular polysaccharide export inner membrane	1.020	3.88E-03
	26A9						
		lcbB (Nm)	37(50)	82	LPS or capsule biosynthesis	1.068	
	9B7	galU			LPS core biosynthesis	1.750	
	25B7	rfbU			LPS O-antigen biosynthesis	0.0014	
	10B11	rmlC	100	15	LPS O-antigen biosynthesis	0.232	
	12D5	rfbN			LPS O-antigen biosynthesis	0.024	
	21B8	rfbP			LPS O-antigen biosynthesis	0.029	
	15A9	hypothetical glycosyltransferase	37(55)	270	gi:18977170 LPS O-antigen biosynthesis	0.739	
	4D4	lppB (Hs)	46(63)	83	lipoprotein B precursor	1.870	
Metabolism	17A4	ompP2 (Hi)	40(55)	237	Outer membrane protein P2 precursor	1.149	
	10B12	adpP (Hi)	61(76)	62	ADP-ribose pyrophosphatase	1.029	
	10A11	argG (Hi)	65(88)	34	arginosuccinate synthase	0.802	
	33C7	atpA (Hi)	89(95)	134	ATP synthase	0.314	
	17B8	ccmH (Hi)	53(77)	166	cytochrome C biogenesis protein	1.100	
	35D11	dsbA (Hi)	63(77)	160	thiol:disulphide interchange protein precursor	1.040	3.43E-04
	26C3	hemA (Pm)	61(74)	394	Glutamyl-tRNA reductase	0.048	
	4B9	moaA (Hi)	67(74)	114	molybdenum cofactor biosynthesis protein	1.150	

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19D5	mnp					AAD01696	ATPase	0.200	
29B11	napB (Pm)	55(70)	77	AAK03681	periplasmic nitrate reductase	1.050		1.093	
9B5	pnp (Pm)	75(79)	125	AAF68421	polynucleotide phosphorylase	1.180			
0A7	pntB (Hi)	68(77)	458	P43010	NAD(P) transhydrogenase	0.785			
23C9	aopA/nqrA			AAC43631	Na-translocating NADH-ubiquinone oxidoreductase	0.716			
29A10	prfC (Hi)	73(81)	342	P43928	peptide chain release factor	4.670			
29B12	recR (Hi)	81(87)	71	P44712	Recombination protein	3.600			
26A10	thrC (Hi)	88(93)	190	P44503	Threonine synthase	0.867		1.598	
0F6	tonB (Hd)	64(74)	288	O51810	Energy transducer	2.488		2.20E-02	
27A12	tonB			Y17916	Energy transducer	0.902		1.54	
26D5	uroD/hemE (Pm)	88(93)	230	AAK03818	Uroporphyrinogen decarboxylase	NA*			
15A11	visC (Pm)	55(82)	43	AAK03810	monooxygenase	0.684			
26A6	yibK (Hi)	70(84)	127	P44868	probable tRNA/rRNA methyltransferase	0.599			
33B7	yifH (Hi)	77(85)	157	P44906	probable rRNA methylase	0.744			
26D12	guaA (Hi)	83(85)	43	P44335	GMP synthase	1.586			
6C12	fur (Hd)	79(83)	139	P71333	ferric uptake regulator	0.627		2.76E-02	
26D3	luxS (Hi)	69(84)	118	P44007	autoinducer-2 production protein	2.063			
19B10	mlcA (Pm)	45(69)	61	AAK03872	negative regulator of rpoE	1.725		6.50E-02	
21D3	rpoE (Hi)	81(90)	189	P44790	Sigma factor E	0.789		0.88	

Regulatory

Stress

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13A3	dnaJ (Hd)	85(99)	14	P48208	chaperone protein	0.163	
26B6	htpG (Ec)	69(82)	368	P10413	Heatshock protein	1.251	
13D8	lon (Pm)	74(86)	292	AAK04062	ATP-dependent protease	0.674	
13C1	prc (Pm)	65(79)	290	AAK02353	tail specific protease	1.324	
22A10	tig (Pm)	50(61)	152	AAK04059	Trigger factor involved in cell division	0.851	
9D10	corC (Hi)	66(78)	248	Q57368	Magnesium and cobalt efflux protein	3.380	
19D1	Hypothetical ABC (Pm)	79(89)	110	AAK03812	ABC transporter	1.341	
0C5	Hypothetical membrane protein (Pm)	81(86)	242	P44884	galactoside ATP transporter	0.651	1.80E-02
0D6	Hypothetical ABC (Pm)	56(76)	210	AAK03081	Probable membrane protein	1.268	
32A7		60(73)	370	AAK03080	Probable ABC transporter	0.962	
13B12	yfeB (Pm)	75(86)	185	AAK02483	Iron (III) ATP-binding protein	0.922	
35D1	znuA (Hd)	71(78)	176	AAF00116	periplasmic zinc ABC transporter	0.450	
14D5	No homology A				Unknown	0.953	5.34E-03
2D5	No homology B				Unknown	1.245	1.03E-02
32A11	Unknown (Pm)	31(52)	124	AAK03268	Unknown	2.950	0.991
4C1	Unknown (Pm)	42(59)	327	AAK02354	Unknown	1.110	0.935
9A4	Hypothetical protein (Hi)	53(74)	91	P44027	C4-decarboxylate transport protein homologue	1.018	

Transport

Unknown